Finsmar

1655

Errors Corrected by the STIC Systems Branch

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#9
AUG 09 2002
TECH CENTER 1600/2900

Serial Number: 09/503,758

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically:

  _____
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.
- ☐ Added the mandatory heading and subheadings for "Current Application Data".
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:

  _____
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:

  _____
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

  _____
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included:

  _____
- ☐ Deleted extra, invalid, headings used by an applicant, specifically:

  _____
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as _____.
- ☐ Inserted mandatory headings, specifically: _____
- ☐ Corrected an obvious error in the response, specifically:

  _____
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☐ Corrected an error in the Number of Sequences field, specifically:

  _____
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted ***ending*** stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: _____
- ☑ Other: Seq 3 - inserted hard returns

  _____

  _____

  _____

***Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**

3/1/95

RAW SEQUENCE LISTING DATE: 08/07/2000
PATENT APPLICATION: US/09/503,758 TIME: 16:37:00

Input Set : A:\Pto.amc
Output Set: N:\CRF3\08072000\I503758.raw

<110> APPLICANT: Thilly, William G.
<120> TITLE OF INVENTION: Methods of Identifying Point Mutations
in a Genome
<130> FILE REFERENCE: 2909.1000-004
<140> CURRENT APPLICATION NUMBER: 09/503,758
<141> CURRENT FILING DATE: 2000-02-14
<150> PRIOR APPLICATION NUMBER: PCT/US99/29379
<151> PRIOR FILING DATE: 1999-12-09
<150> PRIOR APPLICATION NUMBER: US 60/111,457
<151> PRIOR FILING DATE: 1998-12-09
<160> NUMBER OF SEQ ID NOS: 3
<170> SOFTWARE: FastSEQ for Windows Version 4.0
<210> SEQ ID NO: 1
<211> LENGTH: 6
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 1
gtcgca 6
<210> SEQ ID NO: 2
<211> LENGTH: 6
<212> TYPE: DNA
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 2
gttgca 6
<210> SEQ ID NO: 3
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic DNA/RNA chimera
<221> NAME/KEY: modified_base
<222> LOCATION: (17)...(17)
<223> OTHER INFORMATION: 2'-0-methyl adenosine
<221> NAME/KEY: modified_base
<222> LOCATION: (18)...(18)
<223> OTHER INFORMATION: gm
<221> NAME/KEY: modified_base
<222> LOCATION: (19)...(20)
<223> OTHER INFORMATION: cm
<221> NAME/KEY: modified_base
<222> LOCATION: (21)...(21)
<223> OTHER INFORMATION: 2'-0-methyl adenosine
<221> NAME/KEY: modified_base
<222> LOCATION: (22)...(22)
<223> OTHER INFORMATION: gm
<221> NAME/KEY: modified_base
<222> LOCATION: (23)...(23)

RAW SEQUENCE LISTING DATE: 08/07/2000
PATENT APPLICATION: US/09/503,758 TIME: 16:37:00

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69 <223> OTHER INFORMATION: cm
71 <221> NAME/KEY: modified_base
72 <222> LOCATION: (24)...(24)
73 <223> OTHER INFORMATION: um
75 <221> NAME/KEY: modified_base
76 <222> LOCATION: (25)...(26)
77 <223> OTHER INFORMATION: gm
79 <221> NAME/KEY: modified_base
80 <222> LOCATION: (32)...(32)
81 <223> OTHER INFORMATION: 2'-0-methyl adenosine
83 <221> NAME/KEY: modified_base
84 <222> LOCATION: (33)...(33)
85 <223> OTHER INFORMATION: gm
87 <221> NAME/KEY: modified_base
88 <222> LOCATION: (34)...(37)
89 <223> OTHER INFORMATION: 2'-0-methyl adenosine
91 <221> NAME/KEY: modified_base
92 <222> LOCATION: (38)...(39)
93 <223> OTHER INFORMATION: cm
95 <221> NAME/KEY: modified_base
96 <222> LOCATION: (40)...(40)
97 <223> OTHER INFORMATION: um
99 <221> NAME/KEY: modified_base
100 <222> LOCATION: (41)...(41)
101 <223> OTHER INFORMATION: gm
103 <223> OTHER INFORMATION: (1)...(16), (27)...(31), (42)...(78) DNA
105 <223> OTHER INFORMATION: (17)...(26), (32)...(41) 2'-0-methyl RNA
107 <400> SEQUENCE: 3
108 gggagctttt gctcccagcc agcuggccta gagaaaaccu gaaggttttc cttcaggttt 60
110 tctctaggcc agctggct 78

VERIFICATION SUMMARY DATE: 08/07/2000
PATENT APPLICATION: US/09/503,758 TIME: 16:37:01

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